

SEQUENCE LISTING

<110> BASF Aktiengesellschaft
 <120> Nucleic acid sequences encoding proteins associated with abiotic stress response
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 <170> PatentIn version 3.1

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 aac gag atc ttc gtc gca tcc aaa acg tac tgt cca tac tgc cat gca 96
 Asn Glu Ile Phe Val Ala Ser Lys Thr Tyr Cys Pro Tyr Cys His Ala
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 gcc cta aac acg ctt ttt gaa aag tta aag gtt ccc agg tcc aaa gtt 144
 Ala Leu Asn Thr Leu Phe Glu Lys Leu Lys Val Pro Arg Ser Lys Val
 35 40 45
 ctg gtt ttg caa ttg aat gac atg aag gaa ggc gca gac att cag gct 192
 Leu Val Leu Gln Leu Asn Asp Met Lys Glu Gly Ala Asp Ile Gln Ala
 50 55 60
 gcg tta tat gag att aat ggc caa aga acc gtg cca aac atc tat att 240
 Ala Leu Tyr Glu Ile Asn Gly Gln Arg Thr Val Pro Asn Ile Tyr Ile
 65 70 75 80
 aat ggt aaa cat att gga ggc aac gac gac ttg cag gaa ttg agg gag 288
 Asn Gly Lys His Ile Gly Gly Asn Asp Asp Leu Gln Glu Leu Arg Glu
 85 90 95
 act ggt gaa ttg gag gaa ttg tta gaa cct att ctt gca aat taa 333
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Ala Leu Asn Thr Leu Phe Glu Lys Leu Lys Val Pro Arg Ser Lys Val
 35 40 45

Leu Val Leu Gln Leu Asn Asp Met Lys Glu Gly Ala Asp Ile Gln Ala
 50 55 60

Ala Leu Tyr Glu Ile Asn Gly Gln Arg Thr Val Pro Asn Ile Tyr Ile
 65 70 75 80

Asn Gly Lys His Ile Gly Gly Asn Asp Asp Leu Gln Glu Leu Arg Glu
 85 90 95

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atc acg ttg ttt gcc aca aga att att gct aaa aga ttt tta tct act 96
 Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
 20 25 30

cca aaa atg gta tcc cag gaa aca gtt gct cac gta aag gat ctg att 144
 Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
 35 40 45

ggc caa aag gaa gtg ttt gtt gca gca aag aca tac tgc cct tac tgt 192
 Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
 50 55 60

aaa gct act ttg tct acc ctg ttc caa gaa ttg aac gtt ccc aaa tcc 240
 Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
 65 70 75 80

aag gcc ctt gtg ttg gaa tta gat gaa atg agc aat ggc tca gag att 288
 Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
 85 90 95

caa gac gct tta gaa gaa atc tcg ggc caa aaa act gta cct aac gta 336
 Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
 100 105 110

tac atc aat ggc aag cac att ggt ggt aac agc gat ttg gaa act ttg 384
 Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
 115 120 125

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 20 25 30

Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
 35 40 45

Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
 50 55 60

Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
 65 70 75 80

Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
 85 90 95

Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
 100 105 110

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Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
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tac tgt tat aaa cgc cac caa gca aga tat tac aca gca gca aaa ctt 96
 Tyr Cys Tyr Lys Arg His Gln Ala Arg Tyr Tyr Thr Ala Ala Lys Leu

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Phe	Gln	Glu	Met	Pro	Val	Ile	Glu	Ile	Asn	Asp	Gln	Glu	Gln	Phe	Thr	
	35						40					45				
tac	cta	act	acc	act	gcg	gcc	ggc	gac	aag	tta	atc	gtg	ctt	tat	ttc	192
Tyr	Leu	Thr	Thr	Thr	Ala	Ala	Gly	Asp	Lys	Leu	Ile	Val	Leu	Tyr	Phe	
	50					55					60					
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His	Thr	Ser	Trp	Ala	Glu	Pro	Cys	Lys	Ala	Leu	Lys	Gln	Val	Phe	Glu	
	65				70					75					80	
gcc	att	agt	aat	gag	cct	tcc	aat	tcc	aac	gtc	tct	ttc	tta	tcc	att	288
Ala	Ile	Ser	Asn	Glu	Pro	Ser	Asn	Ser	Asn	Val	Ser	Phe	Leu	Ser	Ile	
				85					90					95		
gat	gcg	gac	gaa	aac	tcg	gaa	att	tca	gaa	ctt	ttt	gaa	atc	tca	gct	336
Asp	Ala	Asp	Glu	Asn	Ser	Glu	Ile	Ser	Glu	Leu	Phe	Glu	Ile	Ser	Ala	
			100					105					110			
gtt	cca	tat	ttt	atc	ata	att	cac	aaa	ggg	aca	atc	tta	aaa	gaa	tta	384
Val	Pro	Tyr	Phe	Ile	Ile	Ile	His	Lys	Gly	Thr	Ile	Leu	Lys	Glu	Leu	
		115					120					125				
tcc	ggc	gcg	gat	cca	aag	gag	tat	gtg	tct	tta	tta	gaa	gac	tgc	aag	432
Ser	Gly	Ala	Asp	Pro	Lys	Glu	Tyr	Val	Ser	Leu	Leu	Glu	Asp	Cys	Lys	
	130					135					140					
aac	tca	gtc	aat	tcc	gga	tca	tca	caa	act	cat	act	atg	gaa	aat	gca	480
Asn	Ser	Val	Asn	Ser	Gly	Ser	Ser	Gln	Thr	His	Thr	Met	Glu	Asn	Ala	
	145				150					155					160	
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Asn	Val	Asn	Glu	Gly	Ser	His	Asn	Asp	Glu	Asp	Asp	Asp	Asp	Glu	Glu	
				165					170					175		
gag	gaa	gaa	gaa	act	gag	gag	caa	ata	aac	gct	aga	ttg	act	aaa	ttg	576
Glu	Glu	Glu	Glu	Thr	Glu	Glu	Gln	Ile	Asn	Ala	Arg	Leu	Thr	Lys	Leu	
				180				185					190			
gtc	aat	gcc	gcg	ccg	gta	atg	tta	ttt	atg	aag	ggg	agc	ccc	tct	gaa	624
Val	Asn	Ala	Ala	Pro	Val	Met	Leu	Phe	Met	Lys	Gly	Ser	Pro	Ser	Glu	
		195					200					205				
cct	aaa	tgc	ggg	ttt	tcg	aga	caa	ctt	gtg	ggg	atc	ttg	aga	gaa	cat	672
Pro	Lys	Cys	Gly	Phe	Ser	Arg	Gln	Leu	Val	Gly	Ile	Leu	Arg	Glu	His	
	210					215					220					
caa	gta	aga	ttt	ggc	ttc	ttt	gat	ata	tta	aga	gac	gaa	tct	gtt	aga	720
Gln	Val	Arg	Phe	Gly	Phe	Phe	Asp	Ile	Leu	Arg	Asp	Glu	Ser	Val	Arg	
	225				230					235					240	
caa	aac	ttg	aaa	aag	ttt	tct	gaa	tgg	cca	act	ttc	cct	caa	ctt	tat	768
Gln	Asn	Leu	Lys	Lys	Phe	Ser	Glu	Trp	Pro	Thr	Phe	Pro	Gln	Leu	Tyr	
				245					250					255		
ata	aat	ggg	gag	ttt	caa	ggc	ggg	tta	gac	att	atc	aag	gaa	tcc	ttg	816
Ile	Asn	Gly	Glu	Phe	Gln	Gly	Gly	Leu	Asp	Ile	Ile	Lys	Glu	Ser	Leu	
			260					265					270			
gag	gaa	gac	cct	gat	ttt	ttg	cag	cat	gct	ctc	caa	tct	taa			858

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 275 280 285

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 <213> Saccharomyces cerevisiae
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Phe Gln Glu Met Pro Val Ile Glu Ile Asn Asp Gln Glu Gln Phe Thr
 35 40 45

Tyr Leu Thr Thr Thr Ala Ala Gly Asp Lys Leu Ile Val Leu Tyr Phe
 50 55 60

His Thr Ser Trp Ala Glu Pro Cys Lys Ala Leu Lys Gln Val Phe Glu
 65 70 75 80

Ala Ile Ser Asn Glu Pro Ser Asn Ser Asn Val Ser Phe Leu Ser Ile
 85 90 95

Asp Ala Asp Glu Asn Ser Glu Ile Ser Glu Leu Phe Glu Ile Ser Ala
 100 105 110

Val Pro Tyr Phe Ile Ile Ile His Lys Gly Thr Ile Leu Lys Glu Leu
 115 120 125

Ser Gly Ala Asp Pro Lys Glu Tyr Val Ser Leu Leu Glu Asp Cys Lys
 130 135 140

Asn Ser Val Asn Ser Gly Ser Ser Gln Thr His Thr Met Glu Asn Ala
 145 150 155 160

Asn Val Asn Glu Gly Ser His Asn Asp Glu Asp Asp Asp Asp Glu Glu
 165 170 175

Glu Glu Glu Glu Thr Glu Glu Gln Ile Asn Ala Arg Leu Thr Lys Leu
 180 185 190

Val Asn Ala Ala Pro Val Met Leu Phe Met Lys Gly Ser Pro Ser Glu
 195 200 205

Pro Lys Cys Gly Phe Ser Arg Gln Leu Val Gly Ile Leu Arg Glu His

210

215

220

Gln Val Arg Phe Gly Phe Phe Asp Ile Leu Arg Asp Glu Ser Val Arg
 225 230 235 240

Gln Asn Leu Lys Lys Phe Ser Glu Trp Pro Thr Phe Pro Gln Leu Tyr
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Ile Asn Gly Glu Phe Gln Gly Gly Leu Asp Ile Ile Lys Glu Ser Leu
 260 265 270

Glu Glu Asp Pro Asp Phe Leu Gln His Ala Leu Gln Ser
 275 280 285

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 act aca aac gct gct aat aaa ctc att gtc tta tat ttt aaa gct caa 96
 Thr Thr Asn Ala Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
 20 25 30
 tgg gct gat cct tgc aaa act atg agc cag gtg cta gaa gct gtt agt 144
 Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
 35 40 45
 gaa aaa gtt agg caa gag gat gtc cgg ttt tta tca ata gat gca gac 192
 Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp
 50 55 60
 gaa cat cca gaa ata tca gac ctt ttt gag att gca gcc gta cca tac 240
 Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr
 65 70 75 80
 ttc gtc ttc att caa aat ggt act att gta aaa gaa ata tca gcc gca 288
 Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala
 85 90 95
 gat cct aag gag ttt gtg aaa agc tta gaa att ctt tcg aat gct tct 336
 Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser
 100 105 110
 gcc tca cta gcg aac aat gcc aag ggt cct aaa tct acg tct gat gag 384
 Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu
 115 120 125
 gaa agc agc ggg tct tcc gat gat gaa gag gac gaa act gaa gaa gaa 432
 Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu

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Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu			
145	150	155	160
ttc atg aaa gga agc cca tca gaa cct aaa tgc gga ttt tct aga cag			528
Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Gln			
	165	170	175
tta gtt ggt atc ctc aga gaa cac caa ata agg ttc gga ttt ttt gat			576
Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asp			
	180	185	190
ata tta aga gac gaa aac gtt aga caa agc ttg aag aag ttt tct gat			624
Ile Leu Arg Asp Glu Asn Val Arg Gln Ser Leu Lys Lys Phe Ser Asp			
	195	200	205
tgg cct act ttt cct cag tta tat atc aat ggg gag ttc cag gga ggt			672
Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly			
	210	215	220
ttg gat att atc aag gaa tct ata gaa gaa gat cct gaa tat ttc caa			720
Leu Asp Ile Ile Lys Glu Ser Ile Glu Glu Asp Pro Glu Tyr Phe Gln			
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His Ala Leu Gln			

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	20	25	30
Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser			
	35	40	45
Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp			
	50	55	60
Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr			
	65	70	75
Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala			
	85	90	95
Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser			
	100	105	110

Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu
 115 120 125

Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu
 130 135 140

Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu
 145 150 155 160

Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Gln
 165 170 175

Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asp
 180 185 190

Ile Leu Arg Asp Glu Asn Val Arg Gln Ser Leu Lys Lys Phe Ser Asp
 195 200 205

Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly
 210 215 220

Leu Asp Ile Ile Lys Glu Ser Ile Glu Glu Asp Pro Glu Tyr Phe Gln
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His Ala Leu Gln

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 cgg gct aag act ctt ctt cgt tac caa aat cgg atg tat ttg agc aca 96
 Arg Ala Lys Thr Leu Leu Arg Tyr Gln Asn Arg Met Tyr Leu Ser Thr
 20 25 30
 gag ata aga aaa gct att gaa gat gcc atc gaa tcg gct cca gtg gtt 144
 Glu Ile Arg Lys Ala Ile Glu Asp Ala Ile Glu Ser Ala Pro Val Val
 35 40 45
 ctt ttc atg aaa ggt act cct gaa ttt ccc aag tgt gga ttt tca aga 192
 Leu Phe Met Lys Gly Thr Pro Glu Phe Pro Lys Cys Gly Phe Ser Arg
 50 55 60

gca acc att gga tta tta gga aat caa ggc gtt gac ccg gcc aaa ttt 240
 Ala Thr Ile Gly Leu Leu Gly Asn Gln Gly Val Asp Pro Ala Lys Phe
 65 70 75 80

gcg gct tat aat gtt tta gaa gac cca gag cta cgt gaa ggt atc aaa 288
 Ala Ala Tyr Asn Val Leu Glu Asp Pro Glu Leu Arg Glu Gly Ile Lys
 85 90 95

gag ttt tca gaa tgg cca act att cca cag tta tat gta aac aaa gaa 336
 Glu Phe Ser Glu Trp Pro Thr Ile Pro Gln Leu Tyr Val Asn Lys Glu
 100 105 110

ttc att ggt gga tgt gat gtt att aca agt atg gca cgc tct ggt gaa 384
 Phe Ile Gly Gly Cys Asp Val Ile Thr Ser Met Ala Arg Ser Gly Glu
 115 120 125

ttg gcc gat ttg cta gaa gag gca cag gca ttg gta cct gaa gaa gaa 432
 Leu Ala Asp Leu Leu Glu Glu Ala Gln Ala Leu Val Pro Glu Glu Glu
 130 135 140

gaa gaa acc aaa gat cgt tga 453
 Glu Glu Thr Lys Asp Arg
 145 150

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Met Phe Leu Pro Lys Phe Asn Pro Ile Arg Ser Phe Ser Pro Ile Leu
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Arg Ala Lys Thr Leu Leu Arg Tyr Gln Asn Arg Met Tyr Leu Ser Thr
 20 25 30

Glu Ile Arg Lys Ala Ile Glu Asp Ala Ile Glu Ser Ala Pro Val Val
 35 40 45

Leu Phe Met Lys Gly Thr Pro Glu Phe Pro Lys Cys Gly Phe Ser Arg
 50 55 60

Ala Thr Ile Gly Leu Leu Gly Asn Gln Gly Val Asp Pro Ala Lys Phe
 65 70 75 80

Ala Ala Tyr Asn Val Leu Glu Asp Pro Glu Leu Arg Glu Gly Ile Lys
 85 90 95

Glu Phe Ser Glu Trp Pro Thr Ile Pro Gln Leu Tyr Val Asn Lys Glu
 100 105 110

Phe Ile Gly Gly Cys Asp Val Ile Thr Ser Met Ala Arg Ser Gly Glu
 115 120 125

Leu Ala Asp Leu Leu Glu Glu Ala Gln Ala Leu Val Pro Glu Glu Glu
 130 135 140

Glu Glu Thr Lys Asp Arg
 145 150

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 tct ggc gac aag tta gtc gtt gtt gac ttt ttt gcc aca tgg tgt ggg 96
 Ser Gly Asp Lys Leu Val Val Val Asp Phe Phe Ala Thr Trp Cys Gly
 20 25 30
 cca tgt aaa atg att gca cca atg att gaa aag ttt gca gaa caa tat 144
 Pro Cys Lys Met Ile Ala Pro Met Ile Glu Lys Phe Ala Glu Gln Tyr
 35 40 45
 tct gac gct gct ttt tac aag ttg gat gtt gat gaa gtc tca gat gtt 192
 Ser Asp Ala Ala Phe Tyr Lys Leu Asp Val Asp Glu Val Ser Asp Val
 50 55 60
 gct caa aaa gct gaa gtt tct tcc atg cct acc cta atc ttc tac aag 240
 Ala Gln Lys Ala Glu Val Ser Ser Met Pro Thr Leu Ile Phe Tyr Lys
 65 70 75 80
 ggc ggt aag gag gtt acc aga gtc gtc ggt gcc aac cca gct gct atc 288
 Gly Gly Lys Glu Val Thr Arg Val Val Gly Ala Asn Pro Ala Ala Ile
 85 90 95
 aag caa gct att gct tcc aac gta tagttgccgg tatattaacg ctacgtaaaag 342
 Lys Gln Ala Ile Ala Ser Asn Val
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 tacatcatgt ttaccagttt aaataaaciaa ttttaaaaag aaactctatt acatctatct 402
 atcattatatt tcttcattgt ctattgtata tttcatcatc ggtgtaacca agaattgata 462
 aaatgtcagt catgctcttg gtattcaact tacaaggtgc agctttctgc acctttggct 522
 tggcggtcca tgcgac 539

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20 25 30

Pro Cys Lys Met Ile Ala Pro Met Ile Glu Lys Phe Ala Glu Gln Tyr
35 40 45

Ser Asp Ala Ala Phe Tyr Lys Leu Asp Val Asp Glu Val Ser Asp Val
50 55 60

Ala Gln Lys Ala Glu Val Ser Ser Met Pro Thr Leu Ile Phe Tyr Lys
65 70 75 80

Gly Gly Lys Glu Val Thr Arg Val Val Gly Ala Asn Pro Ala Ala Ile
85 90 95

Lys Gln Ala Ile Ala Ser Asn Val
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<213> *Saccharomyces cerevisiae*
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<222> (1)..(309)
<223> THX2

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caa gac aag cta gtt gtc gta gat ttc tac gcc act tgg tgc ggt cca 96
Gln Asp Lys Leu Val Val Val Asp Phe Tyr Ala Thr Trp Cys Gly Pro
20 25 30

tgt aaa atg att gct cca atg att gaa aaa ttc tct gaa caa tac cca 144
Cys Lys Met Ile Ala Pro Met Ile Glu Lys Phe Ser Glu Gln Tyr Pro
35 40 45

caa gct gat ttc tat aaa ttg gat gtc gat gaa ttg ggt gat gtt gca 192
Gln Ala Asp Phe Tyr Lys Leu Asp Val Asp Glu Leu Gly Asp Val Ala
50 55 60

caa aag aat gaa gtt tcc gct atg cca act ttg ctt cta ttc aag aac 240
Gln Lys Asn Glu Val Ser Ala Met Pro Thr Leu Leu Phe Lys Asn
65 70 75 80

ggt aag gaa gtt gca aag gtt gtt ggt gcc aac cca gcg gct att aag 288
Gly Lys Glu Val Ala Lys Val Val Gly Ala Asn Pro Ala Ala Ile Lys
85 90 95

caa gcc att gct gct aat gct taaa 313
Gln Ala Ile Ala Ala Asn Ala

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<210> 14
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 <213> *Saccharomyces cerevisiae*
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 20 25 30

Cys Lys Met Ile Ala Pro Met Ile Glu Lys Phe Ser Glu Gln Tyr Pro
 35 40 45

Gln Ala Asp Phe Tyr Lys Leu Asp Val Asp Glu Leu Gly Asp Val Ala
 50 55 60

Gln Lys Asn Glu Val Ser Ala Met Pro Thr Leu Leu Leu Phe Lys Asn
 65 70 75 80

Gly Lys Glu Val Ala Lys Val Val Gly Ala Asn Pro Ala Ala Ile Lys
 85 90 95

Gln Ala Ile Ala Ala Asn Ala
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 <212> DNA
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 <222> (126)..(485)
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 aagag atg ggt tct atg ttc agt gga aat cga ttg aac aag gaa gag atg 170
 Met Gly Ser Met Phe Ser Gly Asn Arg Leu Asn Lys Glu Glu Met
 1 5 10 15
 gag gtt gtc gtg aac aag gcc aaa gag atc gtc tcc gct cac ccg gtc 218
 Glu Val Val Val Asn Lys Ala Lys Glu Ile Val Ser Ala His Pro Val
 20 25 30
 gtt gtc ttc agc aag act tac tgt ggt tat tgc cag agg gtg aaa cag 266
 Val Val Phe Ser Lys Thr Tyr Cys Gly Tyr Cys Gln Arg Val Lys Gln
 35 40 45

ttg ttg aca cag cta ggt gca act ttt aaa gta ctt gag ctc gat gag 314
 Leu Leu Thr Gln Leu Gly Ala Thr Phe Lys Val Leu Glu Leu Asp Glu
 50 55 60
 atg agt gat gga ggt gag atc caa tca gct tta tct gag tgg act gga 362
 Met Ser Asp Gly Gly Glu Ile Gln Ser Ala Leu Ser Glu Trp Thr Gly
 65 70 75
 cag agc act gtt cct aat gtt ttc atc aaa ggc aaa cat atc ggt gga 410
 Gln Ser Thr Val Pro Asn Val Phe Ile Lys Gly Lys His Ile Gly Gly
 80 85 90 95
 tgc gat aga gtg atg gag agt aac aag caa ggc aag ctt gtg cct cta 458
 Cys Asp Arg Val Met Glu Ser Asn Lys Gln Gly Lys Leu Val Pro Leu
 100 105 110
 ctt act gaa gct ggt gct atc tcc aat taactcttcc cagcttgagt 505
 Leu Thr Glu Ala Gly Ala Ile Ser Asn
 115 120
 gaaaactctg aaactataaa cagtggaaat gaagaagaat gttatatgtt acatactgtc 565
 aagtaccccaa ataaggaaag atacttgtgg ttttcacttt gctttaaaca aaacattaac 625
 actgctgtgc tgtttggctc tcctttgtta tg 657

<210> 16
 <211> 120
 <212> PRT
 <213> Brassica napus
 <400> 16

Met Gly Ser Met Phe Ser Gly Asn Arg Leu Asn Lys Glu Glu Met Glu
 1 5 10 15

Val Val Val Asn Lys Ala Lys Glu Ile Val Ser Ala His Pro Val Val
 20 25 30

Val Phe Ser Lys Thr Tyr Cys Gly Tyr Cys Gln Arg Val Lys Gln Leu
 35 40 45

Leu Thr Gln Leu Gly Ala Thr Phe Lys Val Leu Glu Leu Asp Glu Met
 50 55 60

Ser Asp Gly Gly Glu Ile Gln Ser Ala Leu Ser Glu Trp Thr Gly Gln
 65 70 75 80

Ser Thr Val Pro Asn Val Phe Ile Lys Gly Lys His Ile Gly Gly Cys
 85 90 95

Asp Arg Val Met Glu Ser Asn Lys Gln Gly Lys Leu Val Pro Leu Leu
 100 105 110

Thr Glu Ala Gly Ala Ile Ser Asn
 115 120

Ala Gly Ala Glu Lys Ser Val Ala Ala Phe Val Gln Asn Ala Ile Leu
 35 40 45

Ser Asn Lys Ile Val Ile Phe Ser Lys Ser Tyr Cys Pro Tyr Cys Leu
 50 55 60

Arg Ser Lys Arg Ile Phe Arg Glu Leu Lys Glu Gln Pro Phe Val Val
 65 70 75 80

Glu Leu Asp Leu Arg Glu Asp Gly Asp Lys Ile Gln Tyr Glu Leu Leu
 85 90 95

Glu Phe Val Gly Arg Arg Thr Val Pro Gln Val Phe Val Asn Gly Lys
 100 105 110

His Ile Gly Gly Ser Asp Asp Leu Ala Asp Ser Val Glu Asn Gly Gln
 115 120 125

Leu Gln Lys Leu Leu Ala Ala Ser
 130 135

<210> 19
 <211> 672
 <212> DNA
 <213> Brassica napus
 <220>
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 <222> (22)..(540)
 <223> BN1106C2202

<400> 19
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 Met Ala Val Thr Ala Phe Asn Pro Leu Lys
 1 5 10
 ctt gca tct tcg cct cga gat tcg ttt cct tca atc tcc tct tca act 99
 Leu Ala Ser Ser Pro Arg Asp Ser Phe Pro Ser Ile Ser Ser Thr
 15 20 25
 tct tat tcg gtg tct ctg ata agc ttc ggt ttc aga aac tcc gtc gga 147
 Ser Tyr Ser Val Ser Leu Ile Ser Phe Gly Phe Arg Asn Ser Val Gly
 30 35 40
 tct cct ctc aag aaa tgt tct cta aag cag acg tgt tct gtt cga gcc 195
 Ser Pro Leu Lys Lys Cys Ser Leu Lys Gln Thr Cys Ser Val Arg Ala
 45 50 55
 atg tct tct tcg tca ttc gaa tcg ggg atg gag gag agc gtg aag aaa 243
 Met Ser Ser Ser Ser Phe Glu Ser Gly Met Glu Glu Ser Val Lys Lys
 60 65 70
 acg gtg gct gat aac aca gtc gtt gtt tac tcg aaa act tgg tgc cca 291
 Thr Val Ala Asp Asn Thr Val Val Val Tyr Ser Lys Thr Trp Cys Pro
 75 80 85 90

tac tgt tct gaa gtg aag aca ttg ttc aag aga ctt ggt gtt cag cca 339
 Tyr Cys Ser Glu Val Lys Thr Leu Phe Lys Arg Leu Gly Val Gln Pro
 95 100 105

ctg gtg gtt gag ttg gat gaa ctt ggt cca caa ggg aca caa cta cag 387
 Leu Val Val Glu Leu Asp Glu Leu Gly Pro Gln Gly Thr Gln Leu Gln
 110 115 120

aag gta ctg gaa aca ctt act ggg caa cgc act gtt cct aat gtg ttc 435
 Lys Val Leu Glu Thr Leu Thr Gly Gln Arg Thr Val Pro Asn Val Phe
 125 130 135

gtc gga ggc aag cac att ggt ggc tgc aca gat aca gta aac ctg aac 483
 Val Gly Gly Lys His Ile Gly Gly Cys Thr Asp Thr Val Asn Leu Asn
 140 145 150

agg aaa gga gaa ctg gaa ttg atg tta gct gaa gcc aac gct aaa acc 531
 Arg Lys Gly Glu Leu Glu Leu Met Leu Ala Glu Ala Asn Ala Lys Thr
 155 160 165 170

gat cag act tgaggaaatg atggaaactg gctttggaga tgaaccctact 580
 Asp Gln Thr

tctctctctc tctcttttgt aaacattgaa cctcgatttc tctctctaca ctttctagaa 640

catcattcaa ataatacatg aacagaggta aa 672

<210> 20

<211> 173

<212> PRT

<213> Brassica napus

<400> 20

Met Ala Val Thr Ala Phe Asn Pro Leu Lys Leu Ala Ser Ser Pro Arg
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Asp Ser Phe Pro Ser Ile Ser Ser Ser Thr Ser Tyr Ser Val Ser Leu
 20 25 30

Ile Ser Phe Gly Phe Arg Asn Ser Val Gly Ser Pro Leu Lys Lys Cys
 35 40 45

Ser Leu Lys Gln Thr Cys Ser Val Arg Ala Met Ser Ser Ser Ser Phe
 50 55 60

Glu Ser Gly Met Glu Glu Ser Val Lys Lys Thr Val Ala Asp Asn Thr
 65 70 75 80

Val Val Val Tyr Ser Lys Thr Trp Cys Pro Tyr Cys Ser Glu Val Lys
 85 90 95

Thr Leu Phe Lys Arg Leu Gly Val Gln Pro Leu Val Val Glu Leu Asp
 100 105 110

Glu Leu Gly Pro Gln Gly Thr Gln Leu Gln Lys Val Leu Glu Thr Leu
 115 120 125

Thr Gly Gln Arg Thr Val Pro Asn Val Phe Val Gly Gly Lys His Ile
 130 135 140

Gly Gly Cys Thr Asp Thr Val Asn Leu Asn Arg Lys Gly Glu Leu Glu
 145 150 155 160

Leu Met Leu Ala Glu Ala Asn Ala Lys Thr Asp Gln Thr
 165 170

<210> 21
 <211> 627
 <212> DNA
 <213> Brassica napus
 <220>
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 <222> (10)..(411)
 <223> BN1106C2582

<400> 21
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gca cta gtt tca tcc atc tct att gtt tct tcg gct tct tca tcc cct 99
 Ala Leu Val Ser Ser Ile Ser Ile Val Ser Ser Ala Ser Ser Ser Pro
 15 20 25 30

gaa gcc gag ttt gtt aag aag acc atc tct tcc cac aag atc gtt atc 147
 Glu Ala Glu Phe Val Lys Lys Thr Ile Ser Ser His Lys Ile Val Ile
 35 40 45

ttc tcc aaa tcc tac tgc ccg tat tgc agg aga gcc aaa tct gtg ttc 195
 Phe Ser Lys Ser Tyr Cys Pro Tyr Cys Arg Arg Ala Lys Ser Val Phe
 50 55 60

agt gag ctg gat cag gtt cct cat gtt gtg gag ctt gat gaa aga gaa 243
 Ser Glu Leu Asp Gln Val Pro His Val Val Glu Leu Asp Glu Arg Glu
 65 70 75

gat ggg tgg aac gtt cag agt gca ctt gga gag att gtt gga agg cga 291
 Asp Gly Trp Asn Val Gln Ser Ala Leu Gly Glu Ile Val Gly Arg Arg
 80 85 90

aca gta cca cag gtt ttc att aac gga aag cac att gga gga tca gac 339
 Thr Val Pro Gln Val Phe Ile Asn Gly Lys His Ile Gly Gly Ser Asp
 95 100 105 110

gat act gta gaa gcg cat gaa agc ggt gaa ctg gcc aag ctt ctc ggt 387
 Asp Thr Val Glu Ala His Glu Ser Gly Glu Leu Ala Lys Leu Leu Gly
 115 120 125

ctt tcc acc aaa gct gaa ctc tag gttcaatgta gttgtagttg gaggatatt 441
 Leu Ser Thr Lys Ala Glu Leu
 130

caggtgtaag cacttccatt ttccagtttt atgataactt gtaatgtgtt ctgaaggtta 501
 taaacgtctt gtcatagctt tgtgaaacga tattaaaggc tacgagttgg attgagattc 561
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 gggcgg 627

<210> 22
 <211> 133
 <212> PRT
 <213> Brassica napus
 <400> 22

Met Thr Met Met Arg Ser Phe Ser Met Ala Met Leu Leu Val Ala Leu
 1 5 10 15

Val Ser Ser Ile Ser Ile Val Ser Ser Ala Ser Ser Ser Pro Glu Ala
 20 25 30

Glu Phe Val Lys Lys Thr Ile Ser Ser His Lys Ile Val Ile Phe Ser
 35 40 45

Lys Ser Tyr Cys Pro Tyr Cys Arg Arg Ala Lys Ser Val Phe Ser Glu
 50 55 60

Leu Asp Gln Val Pro His Val Val Glu Leu Asp Glu Arg Glu Asp Gly
 65 70 75 80

Trp Asn Val Gln Ser Ala Leu Gly Glu Ile Val Gly Arg Arg Thr Val
 85 90 95

Pro Gln Val Phe Ile Asn Gly Lys His Ile Gly Gly Ser Asp Asp Thr
 100 105 110

Val Glu Ala His Glu Ser Gly Glu Leu Ala Lys Leu Leu Gly Leu Ser
 115 120 125

Thr Lys Ala Glu Leu
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<210> 23
 <211> 743
 <212> DNA
 <213> Brassica napus
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 <222> (42)..(680)
 <223> BN1106C23043

<400> 23
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 Met Gly Gly Ala Val

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5

aag gat att gct tca aag tcc gag ctt gat aac att cgc cag agc ggc	104
Lys Asp Ile Ala Ser Lys Ser Glu Leu Asp Asn Ile Arg Gln Ser Gly	
10 15 20	
gca ccg gtg gtg ctt cac ttc tgg gct tcg tgg tgt gat gct tcg aag	152
Ala Pro Val Val Leu His Phe Trp Ala Ser Trp Cys Asp Ala Ser Lys	
25 30 35	
cag atg gat caa gtc ttc tct cac ctg gct acc gac ttc cct cgc gcc	200
Gln Met Asp Gln Val Phe Ser His Leu Ala Thr Asp Phe Pro Arg Ala	
40 45 50	
cac ttc ttt agg gta gaa gct gag gaa cat cct gag ata tct gaa gct	248
His Phe Phe Arg Val Glu Ala Glu Glu His Pro Glu Ile Ser Glu Ala	
55 60 65	
tac tct gtt tct gct gtt ccc tat ttc gtc ttc ttc aag gat ggc aaa	296
Tyr Ser Val Ser Ala Val Pro Tyr Phe Val Phe Lys Asp Gly Lys	
70 75 80 85	
gct gtg gat aca ctt gag gga gca gat cca tca agt tta gcc aat aaa	344
Ala Val Asp Thr Leu Glu Gly Ala Asp Pro Ser Ser Leu Ala Asn Lys	
90 95 100	
gtt ggc aaa gtc gct ggt tcc agc act tct gct gag cct gct gct cct	392
Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala Glu Pro Ala Ala Pro	
105 110 115	
gca agc cta ggg ctg gct gca ggg cca acg att ctg gaa acc gtc aag	440
Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys	
120 125 130	
gag aat gcg aaa gct act tcg aaa gac cga gct cag cct tta tcc tcc	488
Glu Asn Ala Lys Ala Thr Ser Lys Asp Arg Ala Gln Pro Leu Ser Ser	
135 140 145	
acc acc aag gaa gct ctg aat acc cgt ttg gag aaa ctg acc aac tct	536
Thr Thr Lys Glu Ala Leu Asn Thr Arg Leu Glu Lys Leu Thr Asn Ser	
150 155 160 165	
cac cct gtt atg ttg ttc atg aaa ggt acc cct gag gag cct atg tgc	584
His Pro Val Met Leu Phe Met Lys Gly Thr Pro Glu Glu Pro Met Cys	
170 175 180	
ggt ttc agc aag aac gta gtt aac atc ttg aag gag gag gaa gtt gag	632
Gly Phe Ser Lys Asn Val Val Asn Ile Leu Lys Glu Glu Glu Val Glu	
185 190 195	
ttc gga agt ttc gat ata ctt tcg gac aat gaa gtc cgt gaa ggt ctg	680
Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg Glu Gly Leu	
200 205 210	
aagaagttct tcaactggcc aacgtaccct cagctgtaca gcacggaga gctactctgt	740
gga	743

<210> 24

<211> 213

<212> PRT

<213> Brassica napus

<400> 24

Met Gly Gly Ala Val Lys Asp Ile Ala Ser Lys Ser Glu Leu Asp Asn
 1 5 10 15

Ile Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp
 20 25 30

Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
 35 40 45

Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
 50 55 60

Glu Ile Ser Glu Ala Tyr Ser Val Ser Ala Val Pro Tyr Phe Val Phe
 65 70 75 80

Phe Lys Asp Gly Lys Ala Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
 85 90 95

Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala
 100 105 110

Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile
 115 120 125

Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Thr Ser Lys Asp Arg Ala
 130 135 140

Gln Pro Leu Ser Ser Thr Thr Lys Glu Ala Leu Asn Thr Arg Leu Glu
 145 150 155 160

Lys Leu Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Thr Pro
 165 170 175

Glu Glu Pro Met Cys Gly Phe Ser Lys Asn Val Val Asn Ile Leu Lys
 180 185 190

Glu Glu Glu Val Glu Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu
 195 200 205

Val Arg Glu Gly Leu
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<210> 25

<211> 336

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS
 <222> (1) .. (333)
 <223> AtQ9FM49

<400> 25
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 Met Glu Val Val Val Asn Lys Ala Lys Glu Ile Val Ser Ala Tyr Pro
 1 5 10 15
 gtt gtt gtc ttc agc aag aca tac tgt ggt tat tgc cag agg gtg aag 96
 Val Val Val Phe Ser Lys Thr Tyr Cys Gly Tyr Cys Gln Arg Val Lys
 20 25 30
 cag tta ctg acg cag cta gga gca act ttt aaa gta ctt gag ctc gat 144
 Gln Leu Leu Thr Gln Leu Gly Ala Thr Phe Lys Val Leu Glu Leu Asp
 35 40 45
 gaa atg agt gat gga ggt gag atc caa tca gct tta tca gag tgg act 192
 Glu Met Ser Asp Gly Gly Glu Ile Gln Ser Ala Leu Ser Glu Trp Thr
 50 55 60
 gga cag acc aca gtt cca aac gtc ttc atc aaa gga aac cac atc ggt 240
 Gly Gln Thr Thr Val Pro Asn Val Phe Ile Lys Gly Asn His Ile Gly
 65 70 75 80
 gga tgc gat aga gtg atg gag acc aac aag caa ggc aag ctt gtg cct 288
 Gly Cys Asp Arg Val Met Glu Thr Asn Lys Gln Gly Lys Leu Val Pro
 85 90 95
 cta ctt act gaa gct ggg gct att gca gat aac tct tct caa ctt tga 336
 Leu Leu Thr Glu Ala Gly Ala Ile Ala Asp Asn Ser Ser Gln Leu
 100 105 110

<210> 26
 <211> 111
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 26

Met Glu Val Val Val Asn Lys Ala Lys Glu Ile Val Ser Ala Tyr Pro
 1 5 10 15
 Val Val Val Phe Ser Lys Thr Tyr Cys Gly Tyr Cys Gln Arg Val Lys
 20 25 30
 Gln Leu Leu Thr Gln Leu Gly Ala Thr Phe Lys Val Leu Glu Leu Asp
 35 40 45
 Glu Met Ser Asp Gly Gly Glu Ile Gln Ser Ala Leu Ser Glu Trp Thr
 50 55 60
 Gly Gln Thr Thr Val Pro Asn Val Phe Ile Lys Gly Asn His Ile Gly
 65 70 75 80
 Gly Cys Asp Arg Val Met Glu Thr Asn Lys Gln Gly Lys Leu Val Pro
 85 90 95

Leu Leu Thr Glu Ala Gly Ala Ile Ala Asp Asn Ser Ser Gln Leu
 100 105 110

<210> 27
 <211> 336
 <212> DNA
 <213> Arabidopsis thaliana
 <220>
 <221> CDS
 <222> (1)..(333)
 <223> AtQ9FNE2

<400> 27
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 Met Ala Met Gln Lys Ala Lys Glu Ile Val Asn Ser Glu Ser Val Val
 1 5 10 15
 gtt ttc agc aag act tat tgt cca tat tgc gtg aga gtg aag gag ctt 96
 Val Phe Ser Lys Thr Tyr Cys Pro Tyr Cys Val Arg Val Lys Glu Leu
 20 25 30
 ttg caa caa ttg gga gct aag ttc aag gcc gtt gag ctc gac acc gaa 144
 Leu Gln Gln Leu Gly Ala Lys Phe Lys Ala Val Glu Leu Asp Thr Glu
 35 40 45
 agt gat ggt agc caa att caa tca ggt ctc gca gaa tgg aca gga caa 192
 Ser Asp Gly Ser Gln Ile Gln Ser Gly Leu Ala Glu Trp Thr Gly Gln
 50 55 60
 cgt acc gtg cct aat gtg ttt ata gga gga aat cac atc ggt ggc tgt 240
 Arg Thr Val Pro Asn Val Phe Ile Gly Gly Asn His Ile Gly Gly Cys
 65 70 75 80
 gat gca aca tca aac ttg cat aaa gat ggg aag ttg gtt ccg ctg tta 288
 Asp Ala Thr Ser Asn Leu His Lys Asp Gly Lys Leu Val Pro Leu Leu
 85 90 95
 act gaa gct gga gcg atc gca gga aag act gca aca act tct gct taa 336
 Thr Glu Ala Gly Ala Ile Ala Gly Lys Thr Ala Thr Thr Ser Ala
 100 105 110

<210> 28
 <211> 111
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 28

Met Ala Met Gln Lys Ala Lys Glu Ile Val Asn Ser Glu Ser Val Val
 1 5 10 15
 Val Phe Ser Lys Thr Tyr Cys Pro Tyr Cys Val Arg Val Lys Glu Leu
 20 25 30
 Leu Gln Gln Leu Gly Ala Lys Phe Lys Ala Val Glu Leu Asp Thr Glu
 35 40 45
 Ser Asp Gly Ser Gln Ile Gln Ser Gly Leu Ala Glu Trp Thr Gly Gln

50

55

60

Arg Thr Val Pro Asn Val Phe Ile Gly Gly Asn His Ile Gly Gly Cys
65 70 75 80

Asp Ala Thr Ser Asn Leu His Lys Asp Gly Lys Leu Val Pro Leu Leu
85 90 95

Thr Glu Ala Gly Ala Ile Ala Gly Lys Thr Ala Thr Thr Ser Ala
100 105 110

<210> 29

<211> 393

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1)..(390)

<223> AtQ9FVX1

<400> 29

atg gtt gac cag agt cct cgc cgt gtt gtc gtg gcg gcg ctc cta ttg 48
Met Val Asp Gln Ser Pro Arg Arg Val Val Val Ala Ala Leu Leu Leu
1 5 10 15

ttt gtg gtt ctg tgc gat ctt tcg aat tct gcg gga gct gcg aat tct 96
Phe Val Val Leu Cys Asp Leu Ser Asn Ser Ala Gly Ala Ala Asn Ser
20 25 30

gtg tca gct ttc gtt cag aac gcc atc ttg tcc aac aag att gtc atc 144
Val Ser Ala Phe Val Gln Asn Ala Ile Leu Ser Asn Lys Ile Val Ile
35 40 45

ttc tcc aaa tcc tac tgc ccg tat tgt ttg cgg tcg aaa cgt ata ttc 192
Phe Ser Lys Ser Tyr Cys Pro Tyr Cys Leu Arg Ser Lys Arg Ile Phe
50 55 60

agc caa ctt aag gaa gag cca ttt gtt gtg gag ctt gat cag aga gag 240
Ser Gln Leu Lys Glu Glu Pro Phe Val Val Glu Leu Asp Gln Arg Glu
65 70 75 80

gac gga gat caa atc cag tat gag ctt tta gaa ttc gtt ggt cgt cgt 288
Asp Gly Asp Gln Ile Gln Tyr Glu Leu Leu Glu Phe Val Gly Arg Arg
85 90 95

act gtc ccg caa gtt ttt gtt aac ggc aag cat att ggt gga tca gat 336
Thr Val Pro Gln Val Phe Val Asn Gly Lys His Ile Gly Gly Ser Asp
100 105 110

gat ctt gga gct gct ttg gag agt ggt cag ttg caa aag ctt ctt gct 384
Asp Leu Gly Ala Ala Leu Glu Ser Gly Gln Leu Gln Lys Leu Leu Ala
115 120 125

gca agt tga 393
Ala Ser
130

<210> 30

<211> 130
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 30

Met Val Asp Gln Ser Pro Arg Arg Val Val Val Ala Ala Leu Leu Leu
 1 5 10 15

Phe Val Val Leu Cys Asp Leu Ser Asn Ser Ala Gly Ala Ala Asn Ser
 20 25 30

Val Ser Ala Phe Val Gln Asn Ala Ile Leu Ser Asn Lys Ile Val Ile
 35 40 45

Phe Ser Lys Ser Tyr Cys Pro Tyr Cys Leu Arg Ser Lys Arg Ile Phe
 50 55 60

Ser Gln Leu Lys Glu Glu Pro Phe Val Val Glu Leu Asp Gln Arg Glu
 65 70 75 80

Asp Gly Asp Gln Ile Gln Tyr Glu Leu Leu Glu Phe Val Gly Arg Arg
 85 90 95

Thr Val Pro Gln Val Phe Val Asn Gly Lys His Ile Gly Gly Ser Asp
 100 105 110

Asp Leu Gly Ala Ala Leu Glu Ser Gly Gln Leu Gln Lys Leu Leu Ala
 115 120 125

Ala Ser
 130

<210> 31
 <211> 629
 <212> DNA
 <213> Arabidopsis thaliana
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 <221> CDS
 <222> (48)..(452)
 <223> AtQ9M457

<400> 31
 ccacgcgtcc gtggcatctg aagaagaaga agaagaagaa aggagcc atg aca atg 56
 Met Thr Met
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ttt aga tct atc tcc atg gta atg ctg ctc gtc gca cta gtt aca ttc 104
 Phe Arg Ser Ile Ser Met Val Met Leu Leu Val Ala Leu Val Thr Phe
 5 10 15

att tct atg gtt tct tct gct gct tcg tcc cca gaa gcc gac ttt gtt 152
 Ile Ser Met Val Ser Ser Ala Ala Ser Ser Pro Glu Ala Asp Phe Val
 20 25 30 35


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aag aag act atc tct tcc cat aag atc gtc att ttc tcc aaa tcc tac      200
Lys Lys Thr Ile Ser Ser His Lys Ile Val Ile Phe Ser Lys Ser Tyr
      40                      45                      50

tgc ccc tac tgc aag aaa gct aaa tca gtg ttc aga gag ctg gat caa      248
Cys Pro Tyr Cys Lys Lys Ala Lys Ser Val Phe Arg Glu Leu Asp Gln
      55                      60                      65

gtt cct tat gtt gtc gag ctt gat gaa aga gaa gat ggt tgg agc atc      296
Val Pro Tyr Val Val Glu Leu Asp Glu Arg Glu Asp Gly Trp Ser Ile
      70                      75                      80

cag act gca ctt gga gag att gtt gga agg cga aca gta ccg caa gtc      344
Gln Thr Ala Leu Gly Glu Ile Val Gly Arg Arg Thr Val Pro Gln Val
      85                      90                      95

ttc att aac gga aaa cat ctc gga gga tca gat gat acc gta gat gcg      392
Phe Ile Asn Gly Lys His Leu Gly Gly Ser Asp Asp Thr Val Asp Ala
100                      105                      110                      115

tat gag agc ggt gaa ctc gcc aag ctt ctt ggt gtt tcc ggg aac aaa      440
Tyr Glu Ser Gly Glu Leu Ala Lys Leu Leu Gly Val Ser Gly Asn Lys
      120                      125                      130

gaa gct gaa ctc taggttatat atagttggaa gaattgataa cactctctgt      492
Glu Ala Glu Leu
      135

gatgcttagg tgtaagcaat tcaatttcca tttgtattgt gttctgcagc ttgatcatga      552

ccttgtgaca gcttgatctt gcctttttaa cgtatcttat caaagaccac attctgagtt      612

aaaaaaaaaa aaaaaaa      629

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<210> 32
<211> 135
<212> PRT
<213> Arabidopsis thaliana
<400> 32

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Met Thr Met Phe Arg Ser Ile Ser Met Val Met Leu Leu Val Ala Leu
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Val Thr Phe Ile Ser Met Val Ser Ser Ala Ala Ser Ser Pro Glu Ala
      20                      25                      30

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Asp Phe Val Lys Lys Thr Ile Ser Ser His Lys Ile Val Ile Phe Ser
      35                      40                      45

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Lys Ser Tyr Cys Pro Tyr Cys Lys Lys Ala Lys Ser Val Phe Arg Glu
      50                      55                      60

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Leu Asp Gln Val Pro Tyr Val Val Glu Leu Asp Glu Arg Glu Asp Gly
      65                      70                      75                      80

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Trp Ser Ile Gln Thr Ala Leu Gly Glu Ile Val Gly Arg Arg Thr Val
      85                      90                      95

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Pro Gln Val Phe Ile Asn Gly Lys His Leu Gly Gly Ser Asp Asp Thr
 100 105 110

Val Asp Ala Tyr Glu Ser Gly Glu Leu Ala Lys Leu Leu Gly Val Ser
 115 120 125

Gly Asn Lys Glu Ala Glu Leu
 130 135

<210> 33
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 <212> DNA
 <213> Arabidopsis thaliana
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 <221> CDS
 <222> (1)..(537)
 <223> AtQ9SK75

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 Met Val Ala Ala Thr Val Asn Leu Ala Asn Met Thr Trp Thr Ser Leu
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 aat tca aat cca gca atc tct ttc tcc atg tta agc gga atc aga aac 96
 Asn Ser Asn Pro Ala Ile Ser Phe Ser Met Leu Ser Gly Ile Arg Asn
 20 25 30
 ttg ggc atg tta cct ttc agg aga tgt cta aag ccg aca gtt atc gga 144
 Leu Gly Met Leu Pro Phe Arg Arg Cys Leu Lys Pro Thr Val Ile Gly
 35 40 45
 atc gcg tcg tgg cca cca ctc cgt tgt tct tct gtt aag gct atg tct 192
 Ile Ala Ser Trp Pro Pro Leu Arg Cys Ser Ser Val Lys Ala Met Ser
 50 55 60
 tca tca tcg tct tcg tct gga tcg aca ttg gag gag act gtt aaa acg 240
 Ser Ser Ser Ser Ser Ser Gly Ser Thr Leu Glu Glu Thr Val Lys Thr
 65 70 75 80
 act gtg gca gag aac cct gtc gtt gtt tac tcc aaa acc tgg tgc tca 288
 Thr Val Ala Glu Asn Pro Val Val Val Tyr Ser Lys Thr Trp Cys Ser
 85 90 95
 tac tcg tct caa gtg aag tcc ttg ttc aag agt ctt caa gtt gag cca 336
 Tyr Ser Ser Gln Val Lys Ser Leu Phe Lys Ser Leu Gln Val Glu Pro
 100 105 110
 ctg gtt gtt gaa ttg gat caa ctt ggt tca gaa ggg tcg cag ctg cag 384
 Leu Val Val Glu Leu Asp Gln Leu Gly Ser Glu Gly Ser Gln Leu Gln
 115 120 125
 aat gtg ttg gag aaa att act gga caa tac act gtt ccc aat gtt ttc 432
 Asn Val Leu Glu Lys Ile Thr Gly Gln Tyr Thr Val Pro Asn Val Phe
 130 135 140
 atc gga ggc aag cac att ggt ggc tgc tca gat aca ttg cag ctg cac 480
 Ile Gly Gly Lys His Ile Gly Gly Cys Ser Asp Thr Leu Gln Leu His
 145 150 155 160

aat aaa gga gag ctg gaa gca att tta gct gaa gcc aat gga aaa aac 528
 Asn Lys Gly Glu Leu Glu Ala Ile Leu Ala Glu Ala Asn Gly Lys Asn
 165 170 175

ggt cag acc tag 540
 Gly Gln Thr

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Met Val Ala Ala Thr Val Asn Leu Ala Asn Met Thr Trp Thr Ser Leu
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Asn Ser Asn Pro Ala Ile Ser Phe Ser Met Leu Ser Gly Ile Arg Asn
 20 25 30

Leu Gly Met Leu Pro Phe Arg Arg Cys Leu Lys Pro Thr Val Ile Gly
 35 40 45

Ile Ala Ser Trp Pro Pro Leu Arg Cys Ser Ser Val Lys Ala Met Ser
 50 55 60

Ser Ser Ser Ser Ser Ser Gly Ser Thr Leu Glu Glu Thr Val Lys Thr
 65 70 75 80

Thr Val Ala Glu Asn Pro Val Val Val Tyr Ser Lys Thr Trp Cys Ser
 85 90 95

Tyr Ser Ser Gln Val Lys Ser Leu Phe Lys Ser Leu Gln Val Glu Pro
 100 105 110

Leu Val Val Glu Leu Asp Gln Leu Gly Ser Glu Gly Ser Gln Leu Gln
 115 120 125

Asn Val Leu Glu Lys Ile Thr Gly Gln Tyr Thr Val Pro Asn Val Phe
 130 135 140

Ile Gly Gly Lys His Ile Gly Gly Cys Ser Asp Thr Leu Gln Leu His
 145 150 155 160

Asn Lys Gly Glu Leu Glu Ala Ile Leu Ala Glu Ala Asn Gly Lys Asn
 165 170 175

Gly Gln Thr

<210> 35
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 <223> AtQ9LW13

<400> 35
 atg gcg gct tct tta tcg agc aga ctt ata aaa gga atc gct aat ctc 48
 Met Ala Ala Ser Leu Ser Ser Arg Leu Ile Lys Gly Ile Ala Asn Leu
 1 5 10 15

 aaa gct gtt cgt tct agc aga ttg acg tct gca tca gtc tac caa aat 96
 Lys Ala Val Arg Ser Ser Arg Leu Thr Ser Ala Ser Val Tyr Gln Asn
 20 25 30

 ggg atg atg aga ttt tcc tca aca gtg cca agt gat tca gat aca cat 144
 Gly Met Met Arg Phe Ser Ser Thr Val Pro Ser Asp Ser Asp Thr His
 35 40 45

 gat gat ttc aag cct aca caa aaa gtc cct ccc gat tct acg gac tca 192
 Asp Asp Phe Lys Pro Thr Gln Lys Val Pro Pro Asp Ser Thr Asp Ser
 50 55 60

 ctt aaa gat atc gtt gag aat gat gtg aag gat aat cct gtt atg atc 240
 Leu Lys Asp Ile Val Glu Asn Asp Val Lys Asp Asn Pro Val Met Ile
 65 70 75 80

 tac atg aaa ggt gtc cct gaa tct cct cag tgt ggg ttt agc tca cta 288
 Tyr Met Lys Gly Val Pro Glu Ser Pro Gln Cys Gly Phe Ser Ser Leu
 85 90 95

 gcc gtc aga gtt ttg cag caa tat aat gtt cct atc agt tct aga aac 336
 Ala Val Arg Val Leu Gln Gln Tyr Asn Val Pro Ile Ser Ser Arg Asn
 100 105 110

 att cta gaa gac caa gag ttg aaa aac gct gtg aaa tcc ttc agc cac 384
 Ile Leu Glu Asp Gln Glu Leu Lys Asn Ala Val Lys Ser Phe Ser His
 115 120 125

 tgg cct acg ttt cca cag atc ttc att aag gga gag ttc att ggc ggc 432
 Trp Pro Thr Phe Pro Gln Ile Phe Ile Lys Gly Glu Phe Ile Gly Gly
 130 135 140

 tca gac atc atc ctt aac atg cac aag gaa ggt gaa ttg gag cag aag 480
 Ser Asp Ile Ile Leu Asn Met His Lys Glu Gly Glu Leu Glu Gln Lys
 145 150 155 160

 ctt aaa gac gtc tcc gga aac caa gat tga 510
 Leu Lys Asp Val Ser Gly Asn Gln Asp
 165

<210> 36
 <211> 169
 <212> PRT
 <213> Arabidopsis thaliana
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Met Ala Ala Ser Leu Ser Ser Arg Leu Ile Lys Gly Ile Ala Asn Leu

<400> 37																
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Met	Ala	Leu	Arg	Ser	Val	Lys	Thr	Pro	Thr	Leu	Ile	Thr	Ser	Val	Ala	
				5					10					15		
gtc	gtc	tcc	tcc	tcc	gtt	acc	aac	aag	cct	cac	tct	atc	aga	ttc	tct	96
Val	Val	Ser	Ser	Ser	Val	Thr	Asn	Lys	Pro	His	Ser	Ile	Arg	Phe	Ser	
				20					25					30		
ctt	aaa	cca	acg	tcg	gca	ctc	gtc	gtc	cat	aac	cat	cag	cta	tcg	ttc	144
Leu	Lys	Pro	Thr	Ser	Ala	Leu	Val	Val	His	Asn	His	Gln	Leu	Ser	Phe	

35	40	45	
tac ggt tcg aat ctc aag ctg aaa cca act aaa ttc cga tgc tca gcg Tyr Gly Ser Asn Leu Lys Leu Lys Pro Thr Lys Phe Arg Cys Ser Ala 50 55 60			192
tcg gct ctt acg ccg caa ctt aaa gac acg ctg gag aaa ctg gtg aat Ser Ala Leu Thr Pro Gln Leu Lys Asp Thr Leu Glu Lys Leu Val Asn 65 70 75 80			240
tcg gag aaa gtg gtt ctg ttt atg aaa gga acg aga gac ttc ccg atg Ser Glu Lys Val Val Leu Phe Met Lys Gly Thr Arg Asp Phe Pro Met 85 90 95			288
tgt gga ttc tcc aac act gtg gtt cag att ttg aag aat ctg aat gtt Cys Gly Phe Ser Asn Thr Val Val Gln Ile Leu Lys Asn Leu Asn Val 100 105 110			336
cct ttc gaa gat gtg aat att ctg gag aat gag atg ttg agg caa gga Pro Phe Glu Asp Val Asn Ile Leu Glu Asn Glu Met Leu Arg Gln Gly 115 120 125			384
ctt aaa gag tat tcg aat tgg ccg acg ttt cct cag ctt tat atc ggc Leu Lys Glu Tyr Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Ile Gly 130 135 140			432
ggt gag ttt ttc ggt ggt tgt gat att act ctt gag gcg ttt aag act Gly Glu Phe Phe Gly Gly Cys Asp Ile Thr Leu Glu Ala Phe Lys Thr 145 150 155 160			480
gga gaa ttg cag gaa gag gtg gag aaa gct atg tgc tct tga Gly Glu Leu Gln Glu Glu Val Glu Lys Ala Met Cys Ser 165 170			522

<210> 38
 <211> 173
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 <213> Arabidopsis thaliana
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Met Ala Leu Arg Ser Val Lys Thr Pro Thr Leu Ile Thr Ser Val Ala
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Val Val Ser Ser Ser Val Thr Asn Lys Pro His Ser Ile Arg Phe Ser
20 25 30

Leu Lys Pro Thr Ser Ala Leu Val Val His Asn His Gln Leu Ser Phe
35 40 45

Tyr Gly Ser Asn Leu Lys Leu Lys Pro Thr Lys Phe Arg Cys Ser Ala
50 55 60

Ser Ala Leu Thr Pro Gln Leu Lys Asp Thr Leu Glu Lys Leu Val Asn
65 70 75 80

Ser Glu Lys Val Val Leu Phe Met Lys Gly Thr Arg Asp Phe Pro Met
85 90 95

Cys Gly Phe Ser Asn Thr Val Val Gln Ile Leu Lys Asn Leu Asn Val
 100 105 110

Pro Phe Glu Asp Val Asn Ile Leu Glu Asn Glu Met Leu Arg Gln Gly
 115 120 125

Leu Lys Glu Tyr Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Ile Gly
 130 135 140

Gly Glu Phe Phe Gly Gly Cys Asp Ile Thr Leu Glu Ala Phe Lys Thr
 145 150 155 160

Gly Glu Leu Gln Glu Glu Val Glu Lys Ala Met Cys Ser
 165 170

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 <223> AT080451

<400> 39
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 Met Ala Ala Ile Thr Ile Ser Ser Ser Leu His Ala Ser Ala Ser Pro
 1 5 10 15
 cgt gtt gtt cgt cca cat gtt tct cga aat acc cct gtg atc acc ctc 96
 Arg Val Val Arg Pro His Val Ser Arg Asn Thr Pro Val Ile Thr Leu
 20 25 30
 tat tca cgc ttc aca cca tcc ttc tcc ttc cca tct ctc tcc ttc aca 144
 Tyr Ser Arg Phe Thr Pro Ser Phe Ser Phe Pro Ser Leu Ser Phe Thr
 35 40 45
 ctc cgt gac aca gct ccg tct cgt cgt cgt tcc ttc ttt atc gcc tcc 192
 Leu Arg Asp Thr Ala Pro Ser Arg Arg Arg Ser Phe Phe Ile Ala Ser
 50 55 60
 gcc gtc aaa tct cta acg gag acg gag ctg ctt cca atc aca gag gct 240
 Ala Val Lys Ser Leu Thr Glu Thr Glu Leu Leu Pro Ile Thr Glu Ala
 65 70 75 80
 gat tca atc ccg tcc gct tcc ggt gta tac gct gta tac gat aag agc 288
 Asp Ser Ile Pro Ser Ala Ser Gly Val Tyr Ala Val Tyr Asp Lys Ser
 85 90 95
 gac gag ctt cag ttc gtc gga att tct cgg aac atc gct gcg agt gtc 336
 Asp Glu Leu Gln Phe Val Gly Ile Ser Arg Asn Ile Ala Ala Ser Val
 100 105 110
 tct gct cat ctc aaa tct gtg ccg gag ctt tgt ggc tcc gtt aag gtt 384
 Ser Ala His Leu Lys Ser Val Pro Glu Leu Cys Gly Ser Val Lys Val
 115 120 125

gga ata gta gaa gaa cca gat aaa gca gtt tta aca caa gca tgg aaa 432
 Gly Ile Val Glu Glu Pro Asp Lys Ala Val Leu Thr Gln Ala Trp Lys
 130 135 140

tta tgg ata gaa gaa cat ata aaa gta act gga aaa gtt ccg ccg ggg 480
 Leu Trp Ile Glu Glu His Ile Lys Val Thr Gly Lys Val Pro Pro Gly
 145 150 155 160

aat aag tca ggg aac aac aca ttt gtc aaa caa act ccg agg aag aaa 528
 Asn Lys Ser Gly Asn Asn Thr Phe Val Lys Gln Thr Pro Arg Lys Lys
 165 170 175

tcc gat atc cgt ctc act cca ggt cgc cat gtt gag ctc acg gtt cct 576
 Ser Asp Ile Arg Leu Thr Pro Gly Arg His Val Glu Leu Thr Val Pro
 180 185 190

ttg gag gaa ctg att gac cgt tta gtg aaa gag agc aaa gtg gta gct 624
 Leu Glu Glu Leu Ile Asp Arg Leu Val Lys Glu Ser Lys Val Val Ala
 195 200 205

ttc ata aaa gga tca agg agt gct cct caa tgt gga ttc tca cag aga 672
 Phe Ile Lys Gly Ser Arg Ser Ala Pro Gln Cys Gly Phe Ser Gln Arg
 210 215 220

gtt gtt ggg att ctt gaa agc caa gga gtt gat tat gaa act gtt gat 720
 Val Val Gly Ile Leu Glu Ser Gln Gly Val Asp Tyr Glu Thr Val Asp
 225 230 235 240

gtt ctt gac gat gag tat aat cat ggg cta agg gag acg ctt aag aac 768
 Val Leu Asp Asp Glu Tyr Asn His Gly Leu Arg Glu Thr Leu Lys Asn
 245 250 255

tac agc aat tgg cca acg ttt cca cag ata ttt gtg aaa gga gaa ctt 816
 Tyr Ser Asn Trp Pro Thr Phe Pro Gln Ile Phe Val Lys Gly Glu Leu
 260 265 270

gta gga gga tgt gat att ttg acc tca atg tat gaa aat ggt gaa ctt 864
 Val Gly Gly Cys Asp Ile Leu Thr Ser Met Tyr Glu Asn Gly Glu Leu
 275 280 285

gcc aat atc ttg aac tag 882
 Ala Asn Ile Leu Asn
 290

<210> 40
 <211> 293
 <212> PRT
 <213> Arabidopsis thaliana
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Met Ala Ala Ile Thr Ile Ser Ser Ser Leu His Ala Ser Ala Ser Pro
 1 5 10 15

Arg Val Val Arg Pro His Val Ser Arg Asn Thr Pro Val Ile Thr Leu
 20 25 30

Tyr Ser Arg Phe Thr Pro Ser Phe Ser Phe Pro Ser Leu Ser Phe Thr
 35 40 45

Leu Arg Asp Thr Ala Pro Ser Arg Arg Arg Ser Phe Phe Ile Ala Ser
 50 55 60

Ala Val Lys Ser Leu Thr Glu Thr Glu Leu Leu Pro Ile Thr Glu Ala
 65 70 75 80

Asp Ser Ile Pro Ser Ala Ser Gly Val Tyr Ala Val Tyr Asp Lys Ser
 85 90 95

Asp Glu Leu Gln Phe Val Gly Ile Ser Arg Asn Ile Ala Ala Ser Val
 100 105 110

Ser Ala His Leu Lys Ser Val Pro Glu Leu Cys Gly Ser Val Lys Val
 115 120 125

Gly Ile Val Glu Glu Pro Asp Lys Ala Val Leu Thr Gln Ala Trp Lys
 130 135 140

Leu Trp Ile Glu Glu His Ile Lys Val Thr Gly Lys Val Pro Pro Gly
 145 150 155 160

Asn Lys Ser Gly Asn Asn Thr Phe Val Lys Gln Thr Pro Arg Lys Lys
 165 170 175

Ser Asp Ile Arg Leu Thr Pro Gly Arg His Val Glu Leu Thr Val Pro
 180 185 190

Leu Glu Glu Leu Ile Asp Arg Leu Val Lys Glu Ser Lys Val Val Ala
 195 200 205

Phe Ile Lys Gly Ser Arg Ser Ala Pro Gln Cys Gly Phe Ser Gln Arg
 210 215 220

Val Val Gly Ile Leu Glu Ser Gln Gly Val Asp Tyr Glu Thr Val Asp
 225 230 235 240

Val Leu Asp Asp Glu Tyr Asn His Gly Leu Arg Glu Thr Leu Lys Asn
 245 250 255

Tyr Ser Asn Trp Pro Thr Phe Pro Gln Ile Phe Val Lys Gly Glu Leu
 260 265 270

Val Gly Gly Cys Asp Ile Leu Thr Ser Met Tyr Glu Asn Gly Glu Leu
 275 280 285

Ala Asn Ile Leu Asn
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 <213> Arabidopsis thaliana
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 <222> (1)..(480)
 <223> ATO65541

<400> 41
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 Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Glu Glu Leu Asp Asn
 1 5 10 15
 ttg cgc cac agc gga gca cca ctc gtg ctt cac ttc tgg gct tct tgg 96
 Leu Arg His Ser Gly Ala Pro Leu Val Leu His Phe Trp Ala Ser Trp
 20 25 30
 tgt gac gct tcg aag cag atg gat caa gtt ttc tct cat ctc gct act 144
 Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
 35 40 45
 gat ttc cct cgt gct cac ttc ttt agg gta gaa gct gag gaa cat cct 192
 Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
 50 55 60
 gag ata tct gag gct tat tct gtt gct ctt gtg ccg tat ttc gtc ttc 240
 Glu Ile Ser Glu Ala Tyr Ser Val Ala Leu Val Pro Tyr Phe Val Phe
 65 70 75 80
 ttc aag gat ggc aaa act gtg gat aca ctt gaa ggg gca gat cca tca 288
 Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
 85 90 95
 agt tta gct aat aaa gtt ggc aaa gtt gct ggt tct att act cct gca 336
 Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ile Thr Pro Ala
 100 105 110
 agc tta ggg ttg gct gca ggg cca acg att ctt gaa act gtt aag aag 384
 Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys Lys
 115 120 125
 aat gcg aaa gct tct gga caa gac cga gct cag cct gta tct acc gct 432
 Asn Ala Lys Ala Ser Gly Gln Asp Arg Ala Gln Pro Val Ser Thr Ala
 130 135 140
 gat gct ctc aag aat cgt ttg gaa aaa ctc acc ctg tta tgt tat tca 480
 Asp Ala Leu Lys Asn Arg Leu Glu Lys Leu Thr Leu Leu Cys Tyr Ser
 145 150 155 160
 tga 483

<210> 42
 <211> 160
 <212> PRT
 <213> Arabidopsis thaliana
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Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Glu Glu Leu Asp Asn
 1 5 10 15

Leu Arg His Ser Gly Ala Pro Leu Val Leu His Phe Trp Ala Ser Trp
 20 25 30

Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
 35 40 45

Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
 50 55 60

Glu Ile Ser Glu Ala Tyr Ser Val Ala Leu Val Pro Tyr Phe Val Phe
 65 70 75 80

Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
 85 90 95

Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ile Thr Pro Ala
 100 105 110

Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile Leu Glu Thr Val Lys Lys
 115 120 125

Asn Ala Lys Ala Ser Gly Gln Asp Arg Ala Gln Pro Val Ser Thr Ala
 130 135 140

Asp Ala Leu Lys Asn Arg Leu Glu Lys Leu Thr Leu Leu Cys Tyr Ser
 145 150 155 160

<210> 43
 <211> 1467
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 <223> AtQ9ZPH2

<400> 43

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 Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Ala Glu Leu Asp Asn
 1 5 10 15

ttg cgc cag agc ggc gca cca gtc gtg ctt cac ttc tgg gct tct tgg 96
 Leu Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp
 20 25 30

tgt gat gct tcg aag cag atg gat caa gtt ttc tct cat ctc gct act 144
 Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
 35 40 45

gat ttc cct cgt gct cac ttc ttt agg gtt gaa gct gag gaa cat cct 192
 Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
 50 55 60

gag ata tct gag gct tac tct gtt gct gct gtg cct tat ttc gtc ttc Glu Ile Ser Glu Ala Tyr Ser Val Ala Ala Val Pro Tyr Phe Val Phe 65 70 75 80	240
ttc aag gat ggt aaa act gtg gat aca ctt gag ggt gca gat cca tca Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser 85 90 95	288
agt tta gct aat aag gtt ggc aaa gtt gct ggt tct agt act tct gcg Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala 100 105 110	336
gag cct gct gct cct gca agc tta ggg ttg gct gct ggg cca acg att Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile 115 120 125	384
ctt gaa act gtg aag gag aat gcg aaa gct tct tta caa gac cga gct Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala 130 135 140	432
cag cct gta tct acc gcc gat gct ctc aag agc cgt ttg gaa aag ctc Gln Pro Val Ser Thr Ala Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu 145 150 155 160	480
act aat tct cac cct gtc atg tta ttc atg aaa ggt att cct gaa gag Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Ile Pro Glu Glu 165 170 175	528
cct agg tgt ggg ttt agc agg aaa gta gtt gac att ttg aaa gag gtt Pro Arg Cys Gly Phe Ser Arg Lys Val Val Asp Ile Leu Lys Glu Val 180 185 190	576
aac gtt gat ttt gga agt ttt gac ata cta tcg gat aac gaa gtg cga Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg 195 200 205	624
gag ggt ttg aag aaa ttc tct aac tgg cca acg ttt cct cag ctg tac Glu Gly Leu Lys Lys Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr 210 215 220	672
tgc aac gga gag ctt ctt ggt gga gct gat atc gca ata gcg atg cac Cys Asn Gly Glu Leu Leu Gly Gly Ala Asp Ile Ala Ile Ala Met His 225 230 235 240	720
gag agc ggt gaa cta aaa gat gct ttc aaa gat ctt ggg atc acg aca Glu Ser Gly Glu Leu Lys Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr 245 250 255	768
gtt ggt tca aaa gaa agt cag gat gaa gct gga aaa gga gga ggg gtt Val Gly Ser Lys Glu Ser Gln Asp Glu Ala Gly Lys Gly Gly Gly Val 260 265 270	816
agt tca gga aac aca ggc tta agt gag acc ctc cga gct cgg ctc gaa Ser Ser Gly Asn Thr Gly Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu 275 280 285	864
ggt ctg gtc aat tcc aaa cca gtt atg ctg ttc atg aaa gga aga cca Gly Leu Val Asn Ser Lys Pro Val Met Leu Phe Met Lys Gly Arg Pro 290 295 300	912
gaa gaa cca aag tgt ggg ttc agt ggg aaa gtg gtt gaa atc ctc aac Glu Glu Pro Lys Cys Gly Phe Ser Gly Lys Val Val Glu Ile Leu Asn	960

305	310	315	320	
caa gaa aaa atc gag ttt ggg agt ttc gat atc ctc tta gat gac gaa				1008
Gln Glu Lys Ile Glu Phe Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu				
325		330	335	
gtt cgc caa ggc ctt aaa gtg tat tca aac tgg tca agc tat cct cag				1056
Val Arg Gln Gly Leu Lys Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln				
340	345		350	
ctt tac gtg aaa ggc gag ctt atg ggt gga tca gac att gtc ttg gag				1104
Leu Tyr Val Lys Gly Glu Leu Met Gly Gly Ser Asp Ile Val Leu Glu				
355	360		365	
atg caa aag agc ggt gag ctg aaa aag gtc ttg acc gag aaa ggg atc				1152
Met Gln Lys Ser Gly Glu Leu Lys Lys Val Leu Thr Glu Lys Gly Ile				
370	375		380	
act gga gaa cag agt ctt gaa gat aga ttg aag gca ctg atc aat tcc				1200
Thr Gly Glu Gln Ser Leu Glu Asp Arg Leu Lys Ala Leu Ile Asn Ser				
385	390	395	400	
tcg gaa gta atg cta ttc atg aaa ggt tca cca gat gaa ccg aaa tgc				1248
Ser Glu Val Met Leu Phe Met Lys Gly Ser Pro Asp Glu Pro Lys Cys				
405	410		415	
gga ttt agc tcc aaa gtt gtg aaa gca ttg aga gga gaa aac gtg agt				1296
Gly Phe Ser Ser Lys Val Val Lys Ala Leu Arg Gly Glu Asn Val Ser				
420	425		430	
ttc gga tcg ttt gat atc ttg act gat gaa gaa gta agg caa ggg att				1344
Phe Gly Ser Phe Asp Ile Leu Thr Asp Glu Glu Val Arg Gln Gly Ile				
435	440		445	
aag aat ttc tca aac tgg cca act ttt cct cag cta tac tac aaa ggt				1392
Lys Asn Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Tyr Lys Gly				
450	455		460	
gag tta att gga gga tgt gat atc att atg gag cta agt gag agt ggt				1440
Glu Leu Ile Gly Gly Cys Asp Ile Ile Met Glu Leu Ser Glu Ser Gly				
465	470	475	480	
gat ctc aaa gca act cta tcc gag taa				1467
Asp Leu Lys Ala Thr Leu Ser Glu				
485				

<210> 44
 <211> 488
 <212> PRT
 <213> Arabidopsis thaliana
 <400> 44

Met Ser Gly Thr Val Lys Asp Ile Val Ser Lys Ala Glu Leu Asp Asn
1 5 10 15

Leu Arg Gln Ser Gly Ala Pro Val Val Leu His Phe Trp Ala Ser Trp
20 25 30

Cys Asp Ala Ser Lys Gln Met Asp Gln Val Phe Ser His Leu Ala Thr
35 40 45

Asp Phe Pro Arg Ala His Phe Phe Arg Val Glu Ala Glu Glu His Pro
 50 55 60
 Glu Ile Ser Glu Ala Tyr Ser Val Ala Ala Val Pro Tyr Phe Val Phe
 65 70 75 80
 Phe Lys Asp Gly Lys Thr Val Asp Thr Leu Glu Gly Ala Asp Pro Ser
 85 90 95
 Ser Leu Ala Asn Lys Val Gly Lys Val Ala Gly Ser Ser Thr Ser Ala
 100 105 110
 Glu Pro Ala Ala Pro Ala Ser Leu Gly Leu Ala Ala Gly Pro Thr Ile
 115 120 125
 Leu Glu Thr Val Lys Glu Asn Ala Lys Ala Ser Leu Gln Asp Arg Ala
 130 135 140
 Gln Pro Val Ser Thr Ala Asp Ala Leu Lys Ser Arg Leu Glu Lys Leu
 145 150 155 160
 Thr Asn Ser His Pro Val Met Leu Phe Met Lys Gly Ile Pro Glu Glu
 165 170 175
 Pro Arg Cys Gly Phe Ser Arg Lys Val Val Asp Ile Leu Lys Glu Val
 180 185 190
 Asn Val Asp Phe Gly Ser Phe Asp Ile Leu Ser Asp Asn Glu Val Arg
 195 200 205
 Glu Gly Leu Lys Lys Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr
 210 215 220
 Cys Asn Gly Glu Leu Leu Gly Gly Ala Asp Ile Ala Ile Ala Met His
 225 230 235 240
 Glu Ser Gly Glu Leu Lys Asp Ala Phe Lys Asp Leu Gly Ile Thr Thr
 245 250 255
 Val Gly Ser Lys Glu Ser Gln Asp Glu Ala Gly Lys Gly Gly Gly Val
 260 265 270
 Ser Ser Gly Asn Thr Gly Leu Ser Glu Thr Leu Arg Ala Arg Leu Glu
 275 280 285
 Gly Leu Val Asn Ser Lys Pro Val Met Leu Phe Met Lys Gly Arg Pro

290

295

300

Glu Glu Pro Lys Cys Gly Phe Ser Gly Lys Val Val Glu Ile Leu Asn
 305 310 315 320

Gln Glu Lys Ile Glu Phe Gly Ser Phe Asp Ile Leu Leu Asp Asp Glu
 325 330 335

Val Arg Gln Gly Leu Lys Val Tyr Ser Asn Trp Ser Ser Tyr Pro Gln
 340 345 350

Leu Tyr Val Lys Gly Glu Leu Met Gly Gly Ser Asp Ile Val Leu Glu
 355 360 365

Met Gln Lys Ser Gly Glu Leu Lys Lys Val Leu Thr Glu Lys Gly Ile
 370 375 380

Thr Gly Glu Gln Ser Leu Glu Asp Arg Leu Lys Ala Leu Ile Asn Ser
 385 390 395 400

Ser Glu Val Met Leu Phe Met Lys Gly Ser Pro Asp Glu Pro Lys Cys
 405 410 415

Gly Phe Ser Ser Lys Val Val Lys Ala Leu Arg Gly Glu Asn Val Ser
 420 425 430

Phe Gly Ser Phe Asp Ile Leu Thr Asp Glu Glu Val Arg Gln Gly Ile
 435 440 445

Lys Asn Phe Ser Asn Trp Pro Thr Phe Pro Gln Leu Tyr Tyr Lys Gly
 450 455 460

Glu Leu Ile Gly Gly Cys Asp Ile Ile Met Glu Leu Ser Glu Ser Gly
 465 470 475 480

Asp Leu Lys Ala Thr Leu Ser Glu
 485

<210> 45
 <211> 628
 <212> DNA
 <213> Oryza sativa
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 <221> CDS
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 <223> OZ1116C12744

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atccgggtctc gctatctctc ttccgcacatc cgggacgcg atg gcg gcg ctg ctg 114
Met Ala Ala Leu Leu
1 5

ggc cgg agg ttc ggg atg gcg gcg gcg gcg ctc atc gcc ctc gcg gcg 162
Gly Arg Arg Phe Gly Met Ala Ala Ala Ala Leu Ile Ala Leu Ala Ala
10 15 20

ctc gga tcc gcc gcc tcg ggg acg gcg tcc aag tcg tcc ttc gtg aaa 210
Leu Gly Ser Ala Ala Ser Gly Thr Ala Ser Lys Ser Ser Phe Val Lys
25 30 35

tcc acc gtc aaa gcc cac gac gtc gtc ata ttc tcc aag tca tac tgc 258
Ser Thr Val Lys Ala His Asp Val Val Ile Phe Ser Lys Ser Tyr Cys
40 45 50

ccg tac tgt aga aga gcc aaa gct gtg ttc aag gaa ctt gaa ctg aag 306
Pro Tyr Cys Arg Arg Ala Lys Ala Val Phe Lys Glu Leu Glu Leu Lys
55 60 65

aag gag ccg tat gtt gtg gag ctt gat caa cga gag gat ggt tgg gag 354
Lys Glu Pro Tyr Val Val Glu Leu Asp Gln Arg Glu Asp Gly Trp Glu
70 75 80 85

att cag gat gcc tta tct gac atg gtt ggc agg cga act gtt cct caa 402
Ile Gln Asp Ala Leu Ser Asp Met Val Gly Arg Arg Thr Val Pro Gln
90 95 100

gtt ttt gtc cat ggg aag cac ctg ggt ggc tct gat gat act gtt gaa 450
Val Phe Val His Gly Lys His Leu Gly Gly Ser Asp Asp Thr Val Glu
105 110 115

gca tat gag agt ggc aag cta gcc aaa ctt ttg aac att gat gtc aaa 498
Ala Tyr Glu Ser Gly Lys Leu Ala Lys Leu Leu Asn Ile Asp Val Lys
120 125 130

gaa gat ctt tgagtagtaa tagtttagca tcaatggcag gcctctttca 547
Glu Asp Leu
135

tttccataga acatacccaa atactatgca actatgaatt cttcatagaa tttggctgtg 607

aatgtcctct ttagcccctt t 628

<210> 46
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<212> PRT
<213> Oryza sativa
<400> 46

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1 5 10 15

Ile Ala Leu Ala Ala Leu Gly Ser Ala Ala Ser Gly Thr Ala Ser Lys
20 25 30

Ser Ser Phe Val Lys Ser Thr Val Lys Ala His Asp Val Val Ile Phe
35 40 45

Ser Lys Ser Tyr Cys Pro Tyr Cys Arg Arg Ala Lys Ala Val Phe Lys
 50 55 60

Glu Leu Glu Leu Lys Lys Glu Pro Tyr Val Val Glu Leu Asp Gln Arg
 65 70 75 80

Glu Asp Gly Trp Glu Ile Gln Asp Ala Leu Ser Asp Met Val Gly Arg
 85 90 95

Arg Thr Val Pro Gln Val Phe Val His Gly Lys His Leu Gly Gly Ser
 100 105 110

Asp Asp Thr Val Glu Ala Tyr Glu Ser Gly Lys Leu Ala Lys Leu Leu
 115 120 125

Asn Ile Asp Val Lys Glu Asp Leu
 130 135

<210> 47
 <211> 733
 <212> DNA
 <213> Oryza sativa
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 <221> CDS
 <222> (86)..(466)
 <223> OZ1116C2194

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 Met Gly Ile Ala Ser Ser Ser Ser Ser
 1 5
 acc ccg gaa tcc agg aag atg gcg ctc gcc aag gcc aag gag acc gtc 160
 Thr Pro Glu Ser Arg Lys Met Ala Leu Ala Lys Ala Lys Glu Thr Val
 10 15 20 25
 gcc tcc gct ccc gtc gtc gtc tac agc aag tct tac tgt cct ttt tgc 208
 Ala Ser Ala Pro Val Val Val Tyr Ser Lys Ser Tyr Cys Pro Phe Cys
 30 35 40
 gtc cgt gtg aag aag ttg ttc gag cag ctt gga gca act ttc aag gcc 256
 Val Arg Val Lys Lys Leu Phe Glu Gln Leu Gly Ala Thr Phe Lys Ala
 45 50 55
 att gag ttg gat ggg gag agt gat gga tct gag ctg cag tcg gca ctt 304
 Ile Glu Leu Asp Gly Glu Ser Asp Gly Ser Glu Leu Gln Ser Ala Leu
 60 65 70
 gct gaa tgg act gga caa agg act gtt cca aat gtc ttc atc aat ggg 352
 Ala Glu Trp Thr Gly Gln Arg Thr Val Pro Asn Val Phe Ile Asn Gly
 75 80 85
 aag cat att ggt ggc tgt gat gat act ttg gca ttg aac aat gaa ggg 400
 Lys His Ile Gly Gly Cys Asp Asp Thr Leu Ala Leu Asn Asn Glu Gly
 90 95 100 105

aag ctg gtg cct ctg ctg acc gag gct gga gca att gcc agt tct gca 448
 Lys Leu Val Pro Leu Leu Thr Glu Ala Gly Ala Ile Ala Ser Ser Ala
 110 115 120

aag acg aca atc acc gca tagttcttcg tgggacactg ggactagcct 496
 Lys Thr Thr Ile Thr Ala
 125

tcgttgacct ctttatactg catccattct attagataat aaaggtggat gtttggttgg 556

caagaccatt acttggtgcc gtctagtatc gtgtgatagc tatcctgtgc ccgtgtgaaa 616

ctccttggaac atcaataata tcgtctttgt gatagcagtt cgctgaaaaa aaaaaaaaaa 676

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 733

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 <212> PRT
 <213> Oryza sativa
 <400> 48

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Ala Leu Ala Lys Ala Lys Glu Thr Val Ala Ser Ala Pro Val Val Val
 20 25 30

Tyr Ser Lys Ser Tyr Cys Pro Phe Cys Val Arg Val Lys Lys Leu Phe
 35 40 45

Glu Gln Leu Gly Ala Thr Phe Lys Ala Ile Glu Leu Asp Gly Glu Ser
 50 55 60

Asp Gly Ser Glu Leu Gln Ser Ala Leu Ala Glu Trp Thr Gly Gln Arg
 65 70 75 80

Thr Val Pro Asn Val Phe Ile Asn Gly Lys His Ile Gly Gly Cys Asp
 85 90 95

Asp Thr Leu Ala Leu Asn Asn Glu Gly Lys Leu Val Pro Leu Leu Thr
 100 105 110

Glu Ala Gly Ala Ile Ala Ser Ser Ala Lys Thr Thr Ile Thr Ala
 115 120 125

<210> 49
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<223> primer
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44

44/45

<222> (1)..(46)

<223> primer

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46

<210> 53

<211> 44

<212> DNA

<213> Artificial

<220>

<221> primer

<222> (1)..(44)

<223> primer

<400> 53

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44

<210> 54

<211> 46

<212> DNA

<213> Artificial

<220>

<221> primer

<222> (1)..(46)

<223> primer

<400> 54

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46

<210> 55

<211> 38

<212> DNA

<213> Artificial

<220>

<221> cloningcassette

<222> (1)..(38)

<223> cloning cassette

<400> 55

ggaattccag ctgaccacca tggcaattcc cggggatc

38